



Bioproduction of butanol from biomass: from genes to bioreactors

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Butanol is produced chemically using either the oxo process starting from propylene (with H₂ and CO over a rhodium catalyst) or the aldol process starting from acetaldehyde. The key problems associated with the bioproduction of butanol are the cost of substrate and butanol toxicity/inhibition of the fermenting microorganisms, resulting in a low butanol titer in the fermentation broth. Recent interest in the production of biobutanol from biomass has led to the re-examination of acetone-butanol-ethanol (ABE) fermentation, including strategies for reducing or eliminating butanol toxicity to the culture and for manipulating the culture to achieve better product specificity and yield. Advances in integrated fermentation and in situ product removal processes have resulted in a dramatic reduction of process streams, reduced butanol toxicity to the fermenting microorganisms, improved substrate utilization, and overall improved bioreactor performance.

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Introduction

Anaerobic bacteria such as the solventogenic clostridia are capable of converting a wide range of carbon sources (e.g. glucose, galactose, cellobiose, mannose, xylose and arabinose) to fuels and chemicals such as butanol, acetone, and ethanol [1**]. However, butanol toxicity to the fermenting microorganisms limits its concentration in the fermentation broth, resulting in low butanol yields and a high cost for butanol recovery from the dilute solutions. During the past decade, the application of molecular techniques to the solventogenic clostridia — combined with recent advances in fermentation techniques — have resulted in the development of a hyper-butanol-producing strain and an

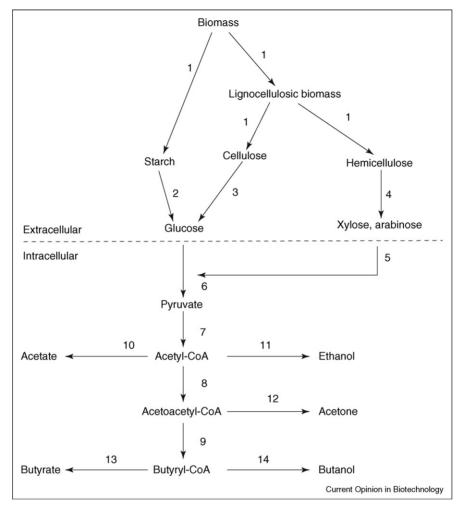
integrated acetone-butanol-ethanol (ABE) fermentation system for the simultaneous production and removal of butanol from the fermentation broth [2].

Efforts have been made to understand the mechanisms of sugar transport, regulation of butanol production, butanol tolerance, utilization of lignocellulosic biomass hydrolysates, and cell inhibition by lignocellulosic degradation products, with the aim of improving butanol productivity, titer and yield. Genetic manipulation of the microorganism depends on the development of effective gene transfer and associated systems. Genetic tools for transformation of the solventogenic clostridia have been developed and transformation of this genus with suitable genes coding for active hydrolytic enzymes would increase not only the utilization of a variety of carbon sources but also the efficiency. This review will focus on current advances in biobutanol production with reference to biomass utilization, strain improvement, bioreactor design and operations.

Regulation of carbohydrate utilization in solventogenic clostridia

The solventogenic clostridia have received much attention in recent years, because of their ability to produce industrially relevant chemicals such as butanol and 1,3-propanediol. The clostridia secrete numerous enzymes that facilitate the breakdown of polymeric carbohydrates into monomers (Figure 1). The secreted carbohydratedegrading enzymes include, but are not limited to, α -amylase, α -glucosidase, β -amylase, β -glucosidase, glucoamylase, pullulanase, and amylopullulanase. The various monosaccharides produced are transported into the cell by specific membrane-bound transport systems, and the carbohydrates are subsequently metabolized via glycolysis or the pentose phosphate pathway (Figure 1). This ability to utilize mixed sugars is of particular relevance for the use of inexpensive agricultural by-products and wastes as fermentation substrates, because fermentation substrate is an important factor influencing the cost of biobutanol production [3]. Genomic sequence data of Clostridium acetobutylicum 824 demonstrated the presence of more than 90 genes encoding enzymes involved in the degradation of carbohydrate polymers, including at least 14 distinct families of glycosyl hydrolases [4]. Likewise, the draft genome sequence data for Clostridium beijerinckii 8052 recently made available by the Department of Energy (DOE) Joint Genome Institute suggested that C. beijerinckii 8052 has the genetic potential for utilization of a wide variety of carbohydrates (http://genome.ornl.gov/ microbial/cbei/13may05/fc_Carbohydrate_Metabolism.

Figure 1



Simplified metabolism of biomass by solventogenic clostridia. 1, Pretreatment of corn and lignocellulose; 2, starch hydrolysis (α-amylase, β-amylase, pullulanase, glucoamylase, α-glucosidase); 3, cellulose hydrolysis (cellulases, β-glucosidase); 4, hemicellulose hydrolysis (see Figure 2); 5, xylose/arabinose uptake and subsequent breakdown via the transketolase-transaldolase sequence producing fructose 6-phosphate and glyceraldehydes 3-phosphate with subsequent metabolism by the Embden-Meyerhof-Parnas (EMP) pathway; 6, glucose uptake by the phosphotransferase system (PTS) and conversion to pyruvate by the EMP pathway; 7, pyruvate-ferrodoxin oxidoreductase; 8, thiolase; 9, 3hydroxybutyryl-CoA dehydrogenase, crotonase and butyryl-CoA dehydrogenase; 10, phosphate acetyltransferase and acetate kinase; 11, acetaldehyde dehydrogenase and ethanol dehydrogenase; 12. acetoacetyl-CoA;acetate/butyrate;CoA transferase and acetoacetate decarboxylase; 13, phosphate butyltransferase and butyrate kinase; 14, butyraldehyde dehydrogenase and butanol dehydrogenase.

html). The genes that make up the carbohydrate catabolic operons are usually expressed when the respective substrates are present in the fermentation medium or when the preferred carbon sources are depleted (TC Ezeji and HP Blaschek, unpublished). Therefore, for efficient fermentation of lignocellulosic hydrolysates, it is imperative to heat shock (to induce expression of heat shock proteins that enhance butanol tolerance and production) the solventogenic clostridia in media containing the representative carbohydrates that are present in the fermentation medium [1**]. So far, the solventogenic clostridia have not been shown to directly utilize crystalline cellulose or lignocellulosic biomass as a carbon source. Genome sequence analysis of C. acetobutylicum 824 revealed 11

proteins identified as cellulosome components. Ten of the genes encoding these components are organized in operon-like clusters (CAC910 to CAC919) with a gene order similar to that of C. cellulolyticum and C. cellulovorans [4]; nevertheless, C. acetobutylicum 824 lacks the ability to degrade crystalline cellulose. As part of an effort to induce the expression of cellulase-encoding genes in C. acetobutylicum 824, a certain level of cellulase secretion was induced by the utilization of xylose, lichenan, and cellobiose as fermentation substrates for butanol production [5]. By contrast, the current draft sequence of C. beijerinckii 8052 indicated an absence of native cellulosome-encoding genes. As a consequence, the ability of C. beijerinckii 8052 to degrade cellulose will have to be achieved through the heterologous expression of introduced cellulosome genes from other species. Furthermore, although at least seven genes encoding xylan-degrading enzymes have been identified in C. beijerinckii 8052, recent investigations in our laboratory demonstrated that C. beijerinckii does not have the ability to degrade xylan or arabinoxylan for butanol production (TC Ezeji and HP Blaschek, unpublished).

Butanol fermentation by solventogenic clostridia

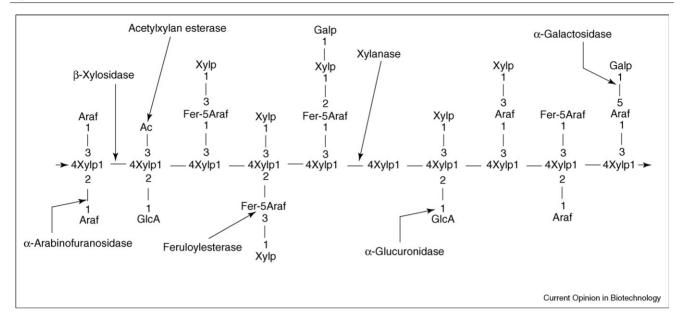
The fermentation profile of a microorganism is ultimately determined by its genetic makeup, which in turn controls the expression of relevant enzymes. An important advantage of the solventogenic clostridia is the variety of fermentation products (acetone, butanol, ethanol, acetic, butyric, lactic acids, etc.) that can be synthesized by this group of microorganisms. However, the loss of available carbon as a result of the formation of unwanted products is an undesirable property of the solventogenic clostridia. Clearly, enzyme synthesis and control of electron flow in the glycolytic pathway are vital with respect to the regulation of the butanol fermentation pathways. The presence of ferrodoxin (Figure 1; 7) is common among the solventogenic clostridia and the direction of electron flow around reduced ferrodoxin could have a crucial impact on the type and quantity of fermentation products produced. In addition, the ability of the solventogenic clostridia to grow under a low redox potential enables them to undertake a variety of stereospecific reductions, yielding chiral products that are difficult to synthesize chemically [6]. As the electron flow can be reversed, butanol yield should respond to factors that influence the direction of electron flow [7]. This observation has caused researchers to test the effect of numerous reducing compounds, such as carbon monoxide gassing, addition of methyl viologen, and the addition of neutral red into the fermentation medium during the ABE fermentation. In the presence of these electron carriers, butanol and ethanol formation were stimulated at the expense of acetone synthesis [7]. In addition, a completely different product, 1,3-propanediol, was synthesized by C. acetobutylicum 824 and C. butyricum VPI 3266 when glycerol, which is a more reduced substrate than glucose, was used as the carbon source [8]. Therefore, the development of an optimal fermentation medium and process for biobutanol production lies in our understanding of the physiology of the bacterium and associated critical interactions between carbon pathways and electron flow.

In the past few years, several carbon sources, such as glucose, starch, corn, molasses and soy molasses, have been utilized for laboratory biobutanol production. As substrate cost has a dramatic influence on butanol price [3], we have recently focused our research on the use of agricultural residues for biobutanol production when using C. beijerinckii BA101. In particular, we have focused on the use of corn stover, corn fiber, and fiber-rich distillers dried grains

and solubles (DDGS) as substrates for butanol fermentation. Although research on the genetics, fermentation, and downstream processing has progressed significantly in recent years, the solventogenic clostridia are not able to efficiently hydrolyze fiber-rich agricultural residues. For this reason, agricultural biomass must be pretreated and hydrolyzed to simple sugars using economical methods. Unfortunately, during pretreatment and hydrolysis, a complex mixture of microbial inhibitors is generated [1^{••}]. Various pretreatment methods such as the use of dilute acid [9], hot water controlled pH [10], and ammonia fiber expansion (AFEX) [11°] are now available to solubilize and depolymerize biomass. Dilute acid pretreatment methods generate significant microbial inhibitors, while hot water and AFEX pretreatment methods generate only low concentrations of inhibitors. Complete hydrolysis of hemicellulose requires xylanase, β-xylosidase, and several other complimentary enzymes, such as acetylxylan esterase, α -arabinofuranosidase, α -glucuronidase, α -galactosidase, ferulic and/or p-coumaric acid esterase (Figure 2). The activities of these enzymes, in addition to the activities of cellulases on the cellulose component of the biomass, result in the generation of complex mixture of acids (e.g. ferulic, p-coumaric, acetic, glucuronic) in addition to monomeric sugars such as glucose, galactose, xylose, and arabinose in the biomass hydrolysates. Compounds such as ferulic and p-coumaric acids have been found to be inhibitory to the solventogenic clostridia at concentrations as low as 0.3 g/L [1**]. The undesirable lignocellulosic hydrolysate components can be divided into three groups on the basis of their origin: compounds released from the hemicellulose component (e.g. acetic, ferulic, glucuronic, p-coumaric acids, etc; Figure 2); lignin degradation products (e.g. syringaldehyde, syringic acid, etc); and sugar degradation products (e.g. furfural, hydroxymethyl furfural [HMF], and levulinic acid). Therefore, for complete depolymerization of lignocellulosic biomass, it is difficult to totally avoid the generation of inhibitory compounds irrespective of the pretreatment and hydrolysis method utilized.

Fermentation of this complex mixture of products by alcohol-producing microorganisms remains a challenge. Most bacteria utilize glucose as the preferred carbon source, and only when glucose is limiting are the pentose sugars utilized. From an economic point of view, it would be preferable for the pentose and hexose sugars to be used concurrently for butanol production, rather than sequentially. The solventogenic clostridia have been shown to utilize other sugars, including cellobiose, galactose, mannose, arabinose and xylose [1 ••] (TC Ezeji and HP Blaschek, unpublished). C. beijerinckii BA101 produced the highest concentration of butanol when cellobiose was used as the carbon source, whereas the least amount of butanol was produced when galactose was used [1°]. Sugar transport across the cell membrane is vital for efficient carbon utilization and butanol production. Solventogenic

Figure 2



Schematic depicting the basic structure of corn fiber heteroxylan and the enzymes needed to degrade the polymer to monomeric compounds. Araf, arabinofuranose; Xylp, xylopyranose; Galp, galactopyranose; GlcA, glucuronic acid; Fer, ferulic acid; AC, acetylxylan (Figure adapted from [28].)

clostridia and many anaerobes transport sugars into the cell through the cell membrane using the phosphoenolpyruvate-dependent phosphotransferase system (PTS) [12], which is involved in the transfer of a phosphate group from phosphoenolpyruvate (PEP) to the sugar. Although glucose and fructose phosphorylation were supported by PEP, indicating the involvement of a PTS in the uptake of these sugars, galactose appears to be transported by a non-PTS mechanism, because a significant rate of phosphorylation of this sugar was supported by ATP rather than PEP [7]. However, C. beijerinckii BA101 and 8052 have been shown to involve both PTS and non-PTS transport systems simultaneously for the uptake of glucose during fermentation, with the non-PTS system (ATP-dependent glucokinase) predominant during the solventogenic phase when the PTS is repressed [12,13°]. Therefore, it seems likely that galactose uptake occurs by a non-PTS mechanism and that its phosphorylation is catalyzed by galactokinase. Efficient galactose uptake in C. beijerinckii and fermentation to butanol might depend on the expression of galactokinase genes and the activity of galactokinase enzymes (ATP-α- D-galactose-1-phosphate transferase (galactokinase), uridine diphosphoglucose-D-galactose-l-phosphate uridylyl transferase, and uridine diphosphogalactose-4-epimerase) during the acidogenic and solventogenic growth phases. During the fermentation of mixed sugars with solventogenic clostridia (C. beijerinckii BA101, C. acetobutylicum 824, C. beijerinckii P-260, C. butylicum 592 and C. saccharobutylicum 292), all the sugars were utilized concurrently throughout the fermentation, although the rate of sugar utilization was sugar specific [1**] (TC Ezeji and HP Blaschek, unpublished). The concurrent uptake and metabolism of the hexose and pentose sugars is a desirable fermentation characteristic. It should be noted that in addition to being able to ferment both hexose and pentose sugars, the fermenting microorganisms must function in the presence of microbial inhibitors, especially those inhibitory compounds that are part of the hemicellulose structure (Figure 2). Adaptation of solventogenic clostridia in dilute acid hydrolyzed corn fiber medium (containing representative inhibitors) before fermentation has been shown to improve fermentation of lignocellulosic hydrolysates by more than 100% (TC Ezeji and HP Blaschek, unpublished).

Genetic strain improvement

The biobutanol fermentation suffers from several limitations (e.g. low titer, yield and productivity) and improvements in the performance of the solventogenic clostridia are necessary to move biobutanol fermentation research to a competitive commercial position. Several approaches have been employed to improve the performance of solventogenic clostridia with the aim of generating strains that can be used in industrial biobutanol production. Recombinant DNA technology, in addition to traditional mutagenesis and selection, have been employed to modify targeted metabolic pathways in the solventogenic clostridia.

Progress has been made over the past decade with respect to genetic manipulation of the solventogenic clostridia. The ability to induce mutagenesis in microorganisms and to isolate mutants of interest has played a major role in the improvement of not only solventogenic clostridia but other industrially important microbes. Mutagens such as hydrogen peroxide, nalidixic acid, metronidazole, ethyl methanesulfonate, N-methyl-N-nitro-N-nitrosoguanidine, and UV irradiation have been used to induce mutations in solventogenic clostridia; amongst these, direct acting N-methyl-N-nitro-N-nitrosoguanidine appears to work best for the solventogenic clostridia. The mutant C. beijerinckii BA101, known for its stability and hyper-amylolytic and hyper-butanologenic characteristics, was generated in 1991 following treatment with N-methyl-N-nitro-N-nitrosoguanidine (reviewed by Ezeji et al. [2]). In 2003, an attempt was made to increase the butanol/acetone ratio in C. acetobutylicum 824 fermentation using antisense RNA strategies. Tummala et al. [14] performed several experiments using antisense RNA to downregulate the enzymes in the acetone formation pathway (acetoacetate decarboxylase [AADC]) and coenzyme A transferase [CoAT]). Despite significant downregulation of the CoAT gene and the production of substantially lower levels of acetone, there was no redirection of the carbon flux towards butanol synthesis; rather, the butanol level was drastically reduced in the resultant mutants. Another attempt was made to increase the butanol/acetone ratio through overexpression of the alcohol-aldehyde dehydrogenase (aad) gene and downregulation of CoAT using antisense RNA against ctfB (the second CoAT gene on the polycistronic aad-ctfA-ctfB message [15]). Again, the butanol level was drastically reduced in the resultant mutant, while the ethanol concentration was 23-fold higher than the control — the highest ethanol level ever reported in C. acetobutylicum. Although progress has been made, the use of recombinant DNA technology has so far not yielded a hyper-butanol-producing industrial strain, probably because of a lack of understanding of the global regulation of butanol production and the unique physiology of the solventogenic clostridia. As butanol is highly toxic to the solventogenic clostridia, metabolic engineering of various microorganisms not typically associated with butanol production, but resistant to butanol toxicity, has been suggested. In addition, simultaneous fermentation and recovery to relieve butanol toxicity (discussed later) might be the best short-term solution given the currently available solventogenic clostridia strains.

Advanced fermentation techniques and novel downstream processing

Traditionally, batch fermentations were commonly used for butanol production because suitable technologies to address the product toxicity problems associated with ABE fermentation were not available. During the 1940s and 1950s, biobutanol production on an industrial scale (Terre Haute, IN and Peoria, IL) was carried out using large batch fermentors ranging in capacity from $200\,000$ to $800\,000$ L. The industrial process used 8-10%

corn mash, which was cooked for 90 min at 130-133 °C. Sugar cane molasses was also used to produce biobutanol in a commercial plant in South Africa until the early 1980s. It should be noted that at a concentration of approximately 16 g butanol/L, cell growth inhibition and premature termination of the fermentation occurs. Product toxicity results in low butanol concentration in the reactor. In addition, the use of a dilute sugar solution results in large process volumes. Because of these problems, the production of biobutanol on a commercial scale has been considered to be uneconomical. Various substrates can be used to produce butanol including corn (dry grind and wet milling processes), molasses, whey permeate or glucose derived from corn [16]. Biobutanol production is a biphasic fermentation where acetic and butyric acids are produced during the acidogenic phase followed by their conversion into acetone and butanol (solventogenic phase). At the end of the fermentation, cell mass and other suspended solids are removed by centrifugation and can be sold as cattle feed. In several recent approaches, agricultural waste such as packing peanuts (peanut-shaped starch-based packing material), orchard waste [16], DDGS (TC Ezeji, HP Blaschek, unpublished), corn fiber [17], and wheat straw [18°] have been used as substrates.

During the past two decades a significant amount of research has been performed on the use of alternative fermentation and product recovery techniques for biobutanol production. These techniques have involved the use of immobilized and cell recycle continuous bioreactors and alternative product recovery technique (e.g. adsorption, gas stripping, ionic liquids, liquid-liquid extraction, pervaporation, aqueous two-phase separation, supercritical extraction, and perstraction, etc). The application of some of these techniques to the ABE fermentation process is described below.

Immobilized and cell recycle continuous bioreactors

In a biobutanol batch process, reactor productivity is limited to less than 0.50 g/L/h for a number of reasons, including low cell concentration, down time, and product inhibition (reviewed in [19]). In a batch reactor a cell concentration of <4 g/L is normally achieved. The cell concentration inside the bioreactor can be increased by one of two techniques, namely 'immobilization' or 'cell recycle'. In a study to explore different cell supports (e.g. clay brick) for *C. beijerinckii* cells, Qureshi *et al.* [16] were able to improve reactor productivity to 15.8 g/L/h. In another approach, Huang et al. [20] immobilized cells of *C. acetobutylicum* in a fibrous support and used these in a continuous reactor to produce ABE; a productivity of 4.6 g/L/h was obtained. Cell recycle — where cells are returned to the bioreactor using a filter and clear liquid is removed — can also be used to increase cell concentration in the reactor and to improve reactor productivity. Using

this approach, reactor productivities up to 6.5 g/L/h (as compared to <0.5 g/L/h in batch fermentation) were achieved in biobutanol fermentation (reviewed in [19]).

Gas stripping

Gas stripping is a technique that can be applied for *in situ* butanol recovery during the ABE fermentation [19,21,22]. The production of ABE is associated with the generation of gases (CO_2 and H_2). In an attempt to make the process of ABE recovery from the fermentation broth simpler and more economical, these fermentation gases are used to recover butanol during simultaneous fermentation and in situ recovery by gas stripping [19,21,22]. The gases are bubbled through the fermentation broth and then cooled in a condenser. As the gas is bubbled through the fermentor, it captures ABE which is subsequently condensed and collected in a receiver vessel. Once the solvents are condensed, the gas is recycled back to the fermentor to capture more ABE. This process continues until all the sugar in the fermentor is utilized by the culture or the fermentation is terminated. In some cases a separate stripper can be used to strip off solvents, the stripper effluent is then recycled back to the reactor [21]. A schematic diagram of ABE production and recovery by gas stripping has been published elsewhere [23,24]. Table 1 compares some of the selected fermentation parameters obtained in non-integrated and integrated (with product recovery) batch, fed-batch, and continuous systems.

Liquid-liquid extraction

The removal of butanol or ABE from fermentation broth by liquid-liquid extraction is considered an important technique. Usually, a water-insoluble organic extractant is mixed with the fermentation broth. Butanol is more soluble in the organic (extractant) phase than in the aqueous (fermentation broth) phase; therefore, butanol selectively concentrates in the organic phase. As the extractant and fermentation broth are immiscible, the extractant can easily be separated from the fermentation broth after butanol extraction. It should be noted that liquid-liquid extraction is able to extract butanol from the fermentation broth without removing substrates, water or nutrients. The extractant of choice among researchers has been olevl alcohol because it is relatively non-toxic, as well as being a good extractant [19,25].

Perstraction

Several problems are associated with liquid-liquid extraction, such as toxicity to the cells, the formation of an emulsion, loss of extraction solvent, and the accumulation of microbial cells at the extractant and fermentation broth interphase. To solve these concerns, a new technique called 'perstraction' was developed [19]. In a perstractive separation, the fermentation broth and the extractant are separated by a membrane. The membrane contactor provides surface area where the two immiscible phases can exchange butanol. As there is no direct contact between the two phases, extractant toxicity, phase dispersion, emulsion and rag layer formation (i.e. the accumulation of cells at the aqueous-organic interphase) are drastically reduced or eliminated. In such a system, butanol would diffuse preferentially across the membrane, while other components and fermentation intermediates (e.g. acetic and butyric acids) are retained in the aqueous phase [26]. The total mass transport of butanol from the fermentation broth to the organic side depends on the rate of diffusion of butanol across the membrane. The membrane does, however, present a physical barrier that can limit the rate of butanol extraction.

Pervaporation

Pervaporation is a technique that allows the selective removal of volatile compounds from model solution/fermentation broth using a membrane. The membrane is placed in contact with the fermentation broth and the volatile or organic component selectively diffuses through the membrane as a vapour. The compound is then recovered by condensation. In this process, a phase change occurs from liquid to vapor. As it is a selective removal process, the desired component requires a heat of vaporization at the feed temperature. The mechanism by

Table 1 A comparison of novel ABE production systems using glucose as substrate.						
Fermentation process	Culture	Sugar used g/L ^a	Total ABE produced g/L	Yield	ABE productivity (g/L/h)	Ref
Batch (control)	C. beijerinckii BA101	<60	<33	0.38-0.40	0.35	[19]
Product recovery by gas	s stripping:					
Batch	C. beijerinckii BA101	161	75.9	0.47 ^b	0.61	[23]
Fed-batch	C. beijerinckii BA101	500	233	0.47 ^b	1.16	[24]
Continuous	C. beijerinckii BA101	1163	460	0.40	0.91	[22]
Product recovery by per	rvaporation:					
Fed-batch	C. acetobutylicum 824	470°	155	0.31-0.35	0.13-0.26	[19]

^b values are higher than expected.

c calculated value.

which a volatile/organic component is removed by pervaporation is called solution-diffusion. The effectiveness of pervaporation is measured by two parameters: the selectivity (a measure of the selective removal of volatiles) and flux (the rate at which an organic/volatile passes through the membrane per m² membrane area). The details of pervaporation have been reviewed by Qureshi and Blaschek [16] and by Ezeji et al. [19].

Economics of the ABE fermentation

In recent years several economic studies have been performed on the production of butanol from corn (dry corn and wet corn milling) whey permeate, and molasses [19,21]. In these studies it was determined that the distillative recovery of biobutanol from the fermentation broth is not economical when compared with butanol derived from the current petrochemical route. Nevertheless, studies employing C. beijerinckii BA101, C. acetobutylicum P260, hydrolyzed DDGS and wheat straw suggest that commercial production of biobutanol from agricultural byproducts/wastes is drawing closer. Recently, DuPont (US) and BP (UK) announced their plans to invest in biobutanol production research. It is anticipated that the first plants would operate on sugar or corn starch; however, it is likely that agricultural waste would become a potential substrate in the near future.

Several recent advances have been made including the development of microbial cultures, process technologies, and use of waste substrates; however, these advances will need to be further developed to run a fermentation-based biobutanol industry that can compete effectively with petrochemically derived butanol. It is suggested that future research might focus on the development of second-generation cultures (as compared to the existing strains C. beijerinckii BA101, C. acetobutylicum PJC4BK, and C. acetobutylicum P260, which produce total ABE on the order of 25-33 g/L [16,19]). Another avenue where technological advances could be made involves the recovery of fermentation by-products (large waste water streams, cell mass, CO₂, and H₂) for further revenue. For example, CO₂ can be converted to algal biomass and oil in the presence of sunlight; use of this zero cost substrate (CO₂) would benefit the biobutanol industry significantly. Additionally, H₂ gas can be separated and used as an excellent source of energy.

Conclusions

The use of lignocellosic biomass as a substrate for biobutanol fermentation has great potential. Much progress has been made with the use of DDGS (TC Ezeji, HP Blaschek, unpublished), wheat straw [18**], and corn fiber xylan [27^{••}]. Nevertheless, to use substrates such as corn fiber hydrolysate and to meet the economic challenges associated with this fermentation, new strains that are both capable of utilizing mixtures of lignocellulosicderived sugars and resistant to microbial inhibitors

present in the lignocellulosic hydrolysate need to be developed. Alternately, economic methods for the removal of inhibitors from these hydrolysates could also be developed. Biobutanol fermentation technology has been changing at a rapid pace. In the authors' opinion, the production of biobutanol using biomass is getting closer to scale-up and possible commercialization. The use of lignocellulosic substrates in combination with developed process technology is expected to make the production of biobutanol economically viable.

Acknowledgements

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This research article demonstrates the effect of compounds such as salts, furfural, hydroxymethyl furfural (HMF), acids (acetic, ferulic, glucuronic, pcoumaric), and phenolic compounds, which are potential degradation products generated during lignocellulosic biomass pretreatment and hydrolysis on cell growth and butanol production. Some of these inhibitory products negatively affect cell growth and butanol production by Clostridium beijerinckii. Furfural and HMF are not inhibitory to C. beijerinckii; rather they have a stimulatory effect on the growth of the microorganism and ABE production.

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